

CLAIMS

1. A method for the prediction of response to cancer treatment, by the detection of at least 2 markers characterized in that the markers are genes and fragments thereof or genomic nucleic acid sequences that are located on one chromosomal region which is altered in malignant neoplasia.
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2. The method of claim 1 wherein the treatment is an antibody treatment, antihormonal treatment, anti-growth factor treatment, taxol based treatment, anthracyclin based treatment and platinum salt based treatment.
3. The method of claim 1 wherein the treatment includes Herceptin™, trastuzumab or 2C4 antibodies.
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4. The method of claim 1 characterized in that the markers are:
 - a) genes that are located on one or more chromosomal region(s) which is/are altered in malignant neoplasia; and
 - b)
 - 15 i) receptor and ligand; or
 - ii) members of the same signal transduction pathway; or
 - iii) members of synergistic signal transduction pathways; or
 - iv) members of antagonistic signal transduction pathways; or
 - v) transcription factor and transcription factor binding site; or
 - 20 vi) integral parts of heteromeric complexes
5. The method of claim 1 or 2 wherein the malignant neoplasia is breast cancer, ovarian cancer, gastric cancer, colon cancer, esophageal cancer, mesenchymal cancer, bladder cancer or non-small cell lung cancer.
6. The method of any of claims 1 to 5 wherein at least one chromosomal region is defined as the cytogenetic region: 1p13, 1q32, 3p21-p24, 5p13-p14, 8q23-q24, 11q13, 12q13, 17q12-q24, 17q11.2-21.3 or 20q13.
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7. A method for the prediction, diagnosis or prognosis of malignant neoplasia by the detection of at least one marker characterized in that the marker is selected from:

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- a) a polynucleotide or polynucleotide analog comprising at least one of the sequences of SEQ ID NO: 319 to 389;
- b) a polynucleotide or polynucleotide analog which hybridizes under stringent conditions to a polynucleotide specified in (a) and encodes a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3
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- c) a polynucleotide or polynucleotide analog the sequence of which deviates from the polynucleotide specified in (a) and (c) due to the generation of the genetic code encoding a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3
- d) a polynucleotide or polynucleotide analog which represents a specific fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d)
- e) a purified polypeptide encoded by a polynucleotide or polynucleotide analog sequence specified in (a) to (e)
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- f) a purified polypeptide comprising at least one of the sequences of SEQ ID NO: 397 - 467;

Are detected.

8. The method according to any of claims 1 to 6 wherein the markers are selected from:

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- a) a polynucleotide or polynucleotide analog comprising at least one of the sequences of SEQ ID NO: 2 to 6, 8, 9, 11 to 16, 18, 19, 21 to 26, 53 to 76 or 315 to 389
- b) a polynucleotide or polynucleotide analog which hybridizes under stringent conditions to a polynucleotide specified in (a) and encodes a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3
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- c) a polynucleotide or polynucleotide analog the sequence of which deviates from the polynucleotide specified in (a) and (b) due to the generation of the genetic code encoding a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3

- d) a polynucleotide or polynucleotide analog which represents a specific fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (c)
 - e) a purified polypeptide encoded by a polynucleotide sequence or polynucleotide analog specified in (a) to (d)
 - 5 f) A purified polypeptide comprising at least one of the sequences of SEQ ID NO: 27 to 52 or 76 to 98 or 393 to 467
- are detected.
9. A diagnostic kit for conducting the method of claims 1 to 8.